```
<!--StartFragment-->RESULT 1
KIRR2 MOUSE
ID KIRR2 MOUSE
                           Reviewed: 700 AA.
AC Q7TSU7; Q7TQ98;
DT 25-OCT-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-0CT-2003, sequence version 1.
DT 24-JUL-2007, entry version 34.
DE Kin of IRRE-like protein 2 precursor (Kin of irregular chiasm-like
DE protein 2).
GN Name=Kirrel2;
   Mus musculus (Mouse).
os
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC.
    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC.
    Muroidea; Muridae; Murinae; Mus.
OX
    NCBI TaxID=10090;
RN
    [1]
RP
    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC
    TISSUE=Olfactory epithelium;
RX PubMed=15489334; DOI=10.1101/gr.2596504;
RG
    The MGC Project Team;
RT
    "The status, quality, and expansion of the NIH full-length cDNA
RT
    project: the Mammalian Gene Collection (MGC).";
RL
   Genome Res. 14:2121-2127(2004).
RN
    [2]
RP
   NUCLEOTIDE SEQUENCE [MRNA] OF 48-376 (ISOFORM 2), AND TISSUE
RP
    SPECIFICITY.
RX
    MEDLINE=22721688; PubMed=12837264; DOI=10.1016/S0888-7543(03)00110-1;
   Sun C., Kilburn D., Lukashin A., Crowell T., Gardner H., Brundiers R.,
RA
    Diefenbach B., Carulli J.P.;
RT "Kirrel2, a novel immunoglobulin superfamily gene expressed primarily
RT in beta cells of the pancreatic islets.";
RL Genomics 82:130-142(2003).
RN
RP
   INTERACTION WITH NPHS2, AND TISSUE SPECIFICITY.
RC
   STRAIN=Swiss Webster; TISSUE=Brain;
RX PubMed=12424224; DOI=10.1096/fi.02-0242fie;
RA
    Sellin L., Huber T.B., Gerke P., Quack I., Pavenstaedt H., Walz G.;
RT
    "NEPH1 defines a novel family of podocin interacting proteins.";
RI.
   FASEB J. 17:115-117(2003).
CC
    -!- SUBUNIT: Interacts with C-terminus of NPHS2/podocin.
CC
    -!- SUBCELLULAR LOCATION: Membrane; Single-pass type I membrane
CC
        protein (Potential).
CC
    -!- ALTERNATIVE PRODUCTS:
CC
        Event=Alternative splicing; Named isoforms=2;
CC
CC
          IsoId=07TSU7-1; Sequence=Displayed;
CC
        Name=2;
CC
         IsoId=07TSU7-2; Sequence=VSP 011786;
CC
    -!- TISSUE SPECIFICITY: Highly expressed in beta-cells of the
CC
        pancreatic islets. Expressed also in podocytes of kidney
CC
         glomeruli.
CC
    -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC
    -!- SIMILARITY: Contains 5 Ig-like C2-type (immunoglobulin-like)
CC
        domains.
CC
CC
    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC
    Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR
   EMBL; BC052773; AAH52773.1; -; mRNA.
DR EMBL; AY305303; AAP72168.1; -; mRNA.
DR
    UniGene: Mm.113908: -.
```

```
Ensembl; ENSMUSG00000036915; Mus musculus.
DR
    MGI; MGI:2442334; Kirrel2.
DR
    InterPro; IPR013162; CD80_C2-set.
    InterPro; IPR007110; Ig-like.
DR
    InterPro; IPR013783; Ig-like_fold.
DR
    InterPro; IPR013098; Iq_I-set.
DR
DR
    InterPro: IPR003599; Ig sub.
DR
    InterPro; IPR003598; Ig_sub2.
DR
    InterPro; IPR013106; Ig_V-set.
DR
    Gene3D; G3DSA:2.60.40.10; Ig-like_fold; 3.
ΠR
    Pfam; PF08205; C2-set_2; 1.
DR
    Pfam; PF07679; I-set; 2.
DR
    Pfam; PF07686; V-set; 1.
ΠR
    SMART; SM00409; IG; 2.
DR
    SMART; SM00408; IGc2; 1.
DR
    PROSITE; PS50835; IG_LIKE; 4.
PF.
    1: Evidence at protein level;
KW
    Alternative splicing; Glycoprotein; Immunoglobulin domain; Membrane;
KW
    Repeat; Signal; Transmembrane.
FT
    SIGNAL
                         19
                                  Potential.
FT
    CHAIN
                  20
                        700
                                  Kin of IRRE-like protein 2.
FT
                                  /FTId=PRO_0000015097.
FT
    TOPO_DOM
                  20
                        507
                                  Extracellular (Potential).
FT
    TRANSMEM
                 508
                                  Potential.
    TOPO DOM
                 529
                        700
                                  Cvtoplasmic (Potential).
FT
    DOMAIN
                 21
                        115
                                  Iq-like C2-type 1.
FT
    DOMAIN
                 120
                        219
                                  Iq-like C2-type 2.
FT
    DOMAIN
                 224
                        304
                                  Ig-like C2-type 3.
                        391
FT
    DOMAIN
                 309
                                  Ig-like C2-type 4.
FT
    DOMAIN
                 395
                        497
                                  Iq-like C2-type 5.
FΤ
    MOTIF
                 146
                        148
                                  Cell attachment site (Potential).
FT
    CARBOHYD
                 140
                        140
                                  N-linked (GlcNAc. . .) (Potential).
FT
    CARBOHYD
                 298
                        298
                                  N-linked (GlcNAc. . .) (Potential).
FT
    CARBOHYD
                                  N-linked (GlcNAc. . .) (Potential).
                 481
                        481
FT
    DISULFID
                 42
                        100
                                  By similarity.
FT
    DISULFID
                 143
                        201
                                  By similarity.
FΤ
    DISULFID
                 245
                        288
                                  By similarity.
FT
    DISULFID
                 330
                        372
                                  By similarity.
FT
    DISULFID
                 416
                        482
                                  By similarity.
FT
    VAR_SEQ
                        136
                                  Missing (in isoform 2).
                 118
FT
                                  /FTId=VSP_011786.
FT
    CONFLICT
                  48
                         48
                                  R \rightarrow W \text{ (in Ref. 2).}
FΤ
    CONFLICT
                 166
                        166
                                  G -> A (in Ref. 2).
    CONFLICT
                 376
                        376
                                  P -> A (in Ref. 2).
    SEQUENCE
                700 AA; 74529 MW; 5D9404C2E13B18B8 CRC64;
 Query Match
                          99.7%; Score 3678; DB 1; Length 700;
 Best Local Similarity
                          99.6%; Pred. No. 1.3e-224;
 Matches 697; Conservative
                                 2; Mismatches
                                                  1; Indels
                                                                     Gaps
                                                                              0;
            1 MLASALLVFLCCFKGHAGSSPHFLOOPEDMVVLLGEEARLPCALGAYRGLVOWTKDGLAL 60
Qy
            1 MLASALLVFLCCFKGHAGSSPHFLQQPEDMVVLLGEEARLPCALGAYRGLVQWTKDGLAL 60
Db
Qv
           61 GGERDLPGWSRYWISGNSASGOHDLHIKPVELEDEASYECQASQAGLRSRPAQLHVMVPP 120
              61 GGERDLPGWSRYWISGNSASGQHDLHIKPVELEDEASYECQASQAGLRSRPAQLHVMVPP 120
          121 EAPQVLGGPSVSLVAGVPGNLTCRSRGDSRPAPELLWFRDGIRLDASSFHQTTLKDKATG 180
Db
          121 EAPQVLGGPSVSLVAGVPGNLTCRSRGDSRPAPELLWFRDGIRLDGSSFHQTTLKDKATG 180
```

QУ	181	TVENTLFLTPSSHDDGATLICRARSQALPTGRDTAVTLSLQYPPMVTLSAEPQTVQEGEK	240
Db	181	TVENTLFLTPSSHDDGATLICRARSQALPTGRDTAVTLSLQYPPMVTLSAEPQTVQEGEK	240
Qу	241	VTFLCQATAQPPVTGYRWAKGGSPVLGARGPRLEVVADATFLTEPVSCEVSNAVGSANRS	300
Db	241	$\verb VTFLCQATAQPPVTGYRWAKGGSPVLGARGPRLEVVADATFLTEPVSCEVSNAVGSANRS \\$	300
Qy	301	TALEVLYGPILQAKPKSVSVDVGKDASFSCVWRGNPLPRITWTRMGGSQVLSSGPTLRLP	360
Db	301	TALEVLYGPILQAKPKSVSVDVGKDASFSCVWRGNPLPRITWTRMGGSQVLSSGPTLRLP	360
Qy	361	SVALEDAGDYVCRAEPRRTGLGGGKAQARLTVNAPPVVTALQPAPAFLRGPARLQCVVFA	420
Db	361	${\tt SVALEDAGDYVCRAEPRRTGLGGGKAQARLTVNAPPVVTALQPAPAFLRGPARLQCVVFA}$	420
Qy	421	SPAPDSVVWSWDEGFLEAGSLGRFLVEAFPAPEVEGGQGPGLISVLHISGTQESDFTTGF	480
Db	421	${\tt SPAPDSVVWSWDEGFLEAGSLGRFLVEAFPAPEVEGGQGPGLISVLHISGTQESDFTTGF}$	480
Qy	481	NCSARNRLGEGRVQIHLGRRDLLPTVRIVAGAASAATSLLMVITGVVLCCWRHGSLSKQK	540
Db	481	${\tt NCSARNRLGEGRVQIHLGRRDLLPTVRIVAGAASAATSLLMVITGVVLCCWRHGSLSKQK}$	540
Qy	541	NLVRIPGSSEGSSSRGPEEETGSSEDRGPIVHTDHSDLVLEEKEALETKDPTNGYYKVRG	600
Db	541	${\tt NLVRIPGSSEGSSSRGPEEETGSSEDRGPIVHTDHSDLVLEEKEALETKDPTNGYYRVRG}$	600
Qy	601	VSVSLSLGEAPGGGLFLPPPSPIGLPGTPTYYDFKPHLDLVPPCRLYRARAGYLTTPHPR	660
Db	601	VSVSLSLGEAPGGGLFLPPPSPIGLPGTPTYYDFKPHLDLVPPCRLYRARAGYLTTPHPR	660
Qу	661	AFTSYMKPTSFGPPDLSSGTPPFFYATLSPPSHQRLQTHV 700	
Db EndFra</td <td></td> <td>AFTSYMKPTSFGPPELSSGTPPFPYATLSPPSHQRLQTHV 700</td> <td></td>		AFTSYMKPTSFGPPELSSGTPPFPYATLSPPSHQRLQTHV 700	